

1-29-03

A5



1600

RAW SEQUENCE LISTING

DATE: 01/29/2003

PATENT APPLICATION: US/09/835,147A

TIME: 13:55:39

Input Set : A:\2879-US RevsdSeqListing 010303.txt

Output Set: N:\CRF4\01292003\I835147A.raw

3 <110> APPLICANT: Maliszewski, Charles R.
 4 Gayle III, Richard B.
 5 Price, Virginia L.
 6 Gimpel, Steven D.
 8 <120> TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
 10 <130> FILE REFERENCE: 2879-US
 12 <140> CURRENT APPLICATION NUMBER: US 09/835,147A
 13 <141> CURRENT FILING DATE: 2001-04-13
 15 <150> PRIOR APPLICATION NUMBER: US 60/104,585
 16 <151> PRIOR FILING DATE: 1998-10-16
 18 <150> PRIOR APPLICATION NUMBER: US 60/107,466
 19 <151> PRIOR FILING DATE: 1998-11-06
 21 <150> PRIOR APPLICATION NUMBER: US 60/149,010
 22 <151> PRIOR FILING DATE: 1998-08-13
 24 <150> PRIOR APPLICATION NUMBER: PCT/US99/22955
 25 <151> PRIOR FILING DATE: 1999-10-13
 27 <160> NUMBER OF SEQ ID NOS: 37
 29 <170> SOFTWARE: PatentIn version 3.1
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 1599
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Homo sapiens
 36 <220> FEATURE:
 37 <221> NAME/KEY: CDS
 38 <222> LOCATION: (67)..(1596)
 39 <223> OTHER INFORMATION:

P.6

ENTERED

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49 aag aat atc cta gcc atc ctt ggc ttc tcc tct atc ata gct gtg ata      156
50 Lys Asn Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile
51 15              20              25              30
53 gct ttg ctt gct gtg ggg ttg acc cag aac aaa gca ttg cca gaa aac      204
54 Ala Leu Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn
55      35              40              45
57 gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta      252
58 Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu
59      50              55              60
61 tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg      300
62 Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val
63      65              70              75

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65	cat	caa	gta	gaa	gaa	tgc	agg	gtt	aaa	ggt	cct	gga	atc	tca	aaa	ttt	348
66	His	Gln	Val	Glu	Glu	Cys	Arg	Val	Lys	Gly	Pro	Gly	Ile	Ser	Lys	Phe	
67		80					85					90					
69	gtt	cag	aaa	gta	aat	gaa	ata	ggc	att	tac	ctg	act	gat	tgc	atg	gaa	396
70	Val	Gln	Lys	Val	Asn	Glu	Ile	Gly	Ile	Tyr	Leu	Thr	Asp	Cys	Met	Glu	
71	95					100					105					110	
73	aga	gct	agg	gaa	gtg	att	cca	agg	tcc	cag	cac	caa	gag	aca	ccc	gtt	444
74	Arg	Ala	Arg	Glu	Val	Ile	Pro	Arg	Ser	Gln	His	Gln	Glu	Thr	Pro	Val	
75					115					120					125		
77	tac	ctg	gga	gcc	acg	gca	ggc	atg	cgg	ttg	ctc	agg	atg	gaa	agt	gaa	492
78	Tyr	Leu	Gly	Ala	Thr	Ala	Gly	Met	Arg	Leu	Leu	Arg	Met	Glu	Ser	Glu	
79				130					135					140			
81	gag	ttg	gca	gac	agg	gtt	ctg	gat	gtg	gtg	gag	agg	agc	ctc	agc	aac	540
82	Glu	Leu	Ala	Asp	Arg	Val	Leu	Asp	Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	
83			145					150					155				
85	tac	ccc	ttt	gac	ttc	cag	ggg	gcc	agg	atc	att	act	ggc	caa	gag	gaa	588
86	Tyr	Pro	Phe	Asp	Phe	Gln	Gly	Ala	Arg	Ile	Ile	Thr	Gly	Gln	Glu	Glu	
87		160					165					170					
89	ggt	gcc	tat	ggc	tgg	att	act	atc	aac	tat	ctg	ctg	ggc	aaa	ttc	agt	636
90	Gly	Ala	Tyr	Gly	Trp	Ile	Thr	Ile	Asn	Tyr	Leu	Leu	Gly	Lys	Phe	Ser	
91	175					180					185				190		
93	cag	aaa	aca	agg	tgg	ttc	agc	ata	gtc	cca	tat	gaa	acc	aat	aat	cag	684
94	Gln	Lys	Thr	Arg	Trp	Phe	Ser	Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln	
95				195						200				205			
97	gaa	acc	ttt	gga	gct	ttg	gac	ctt	ggg	gga	gcc	tct	aca	caa	gtc	act	732
98	Glu	Thr	Phe	Gly	Ala	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Val	Thr	
99			210					215				220					
101	ttt	gta	ccc	caa	aac	cag	act	atc	gag	tcc	cca	gat	aat	gct	ctg	caa	780
102	Phe	Val	Pro	Gln	Asn	Gln	Thr	Ile	Glu	Ser	Pro	Asp	Asn	Ala	Leu	Gln	
103			225					230				235					
105	ttt	cgc	ctc	tat	ggc	aag	gac	tac	aat	gtc	tac	aca	cat	agc	ttc	ttg	828
106	Phe	Arg	Leu	Tyr	Gly	Lys	Asp	Tyr	Asn	Val	Tyr	Thr	His	Ser	Phe	Leu	
107		240					245					250					
109	tgc	tat	ggg	aag	gat	cag	gca	ctc	tgg	cag	aaa	ctg	gcc	aag	gac	att	876
110	Cys	Tyr	Gly	Lys	Asp	Gln	Ala	Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile	
111	255				260					265				270			
113	cag	gtt	gca	agt	aat	gaa	att	ctc	agg	gac	cca	tgc	ttt	cat	cct	gga	924
114	Gln	Val	Ala	Ser	Asn	Glu	Ile	Leu	Arg	Asp	Pro	Cys	Phe	His	Pro	Gly	
115				275					280					285			
117	tat	aag	aag	gta	gtg	aac	gta	agt	gac	ctt	tac	aag	acc	ccc	tgc	acc	972
118	Tyr	Lys	Lys	Val	Val	Asn	Val	Ser	Asp	Leu	Tyr	Lys	Thr	Pro	Cys	Thr	
119			290					295				300					
121	aag	aga	ttt	gag	atg	act	ctt	cca	ttc	cag	cag	ttt	gaa	atc	cag	ggt	1020
122	Lys	Arg	Phe	Glu	Met	Thr	Leu	Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly	
123			305					310				315					
125	att	gga	aac	tat	caa	caa	tgc	cat	caa	agc	atc	ctg	gag	ctc	ttc	aac	1068
126	Ile	Gly	Asn	Tyr	Gln	Gln	Cys	His	Gln	Ser	Ile	Leu	Glu	Leu	Phe	Asn	
127		320					325				330						
129	acc	agt	tac	tgc	cct	tac	tcc	cag	tgt	gcc	ttc	aat	ggg	att	ttc	ttg	1116

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131 335 340 345 350
133 cca cca ctc cag ggg gat ttt ggg gca ttt tca gct ttt tac ttt gtg 1164
134 Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val
135 355 360 365
137 atg aag ttt tta aac ttg aca tca gag aaa gtc tct cag gaa aag gtg 1212
138 Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
139 370 375 380
141 act gag atg atg aaa aag ttc tgt gct cag cct tgg gag gag ata aaa 1260
142 Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
143 385 390 395
145 aca tct tac gct gga gta aag gag aag tac ctg agt gaa tac tgc ttt 1308
146 Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe
147 400 405 410
149 tct ggt acc tac att ctc tcc ctc ctt ctg caa ggc tat cat ttc aca 1356
150 Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr
151 415 420 425 430
153 gct gat tcc tgg gag cac atc cat ttc att ggc aag atc cag ggc agc 1404
154 Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser
155 435 440 445
157 gac gcc ggc tgg act ttg ggc tac atg ctg aac ctg acc aac atg atc 1452
158 Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
159 450 455 460
161 cca gct gag caa cca ttg tcc aca cct ctc tcc cac tcc acc tat gtc 1500
162 Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val
163 465 470 475
165 ttc ctc atg gtt cta ttc tcc ctg gtc ctt ttc aca gtg gcc atc ata 1548
166 Phe Leu Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile
167 480 485 490
169 ggc ttg ctt atc ttt cac aag cct tca tat ttc tgg aaa gat atg gta 1596
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196 50 55 60
199 Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
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219	Ala	Asp	Arg	Val	Leu	Asp	Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	Tyr	Pro
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224				165						170					175	
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228				180					185					190		
231	Thr	Arg	Trp	Phe	Ser	Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln	Glu	Thr
232			195					200					205			
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236			210				215					220				
239	Pro	Gln	Asn	Gln	Thr	Ile	Glu	Ser	Pro	Asp	Asn	Ala	Leu	Gln	Phe	Arg
240	225					230					235					240
243	Leu	Tyr	Gly	Lys	Asp	Tyr	Asn	Val	Tyr	Thr	His	Ser	Phe	Leu	Cys	Tyr
244				245						250					255	
247	Gly	Lys	Asp	Gln	Ala	Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile	Gln	Val
248				260					265					270		
251	Ala	Ser	Asn	Glu	Ile	Leu	Arg	Asp	Pro	Cys	Phe	His	Pro	Gly	Tyr	Lys
252			275					280					285			
255	Lys	Val	Val	Asn	Val	Ser	Asp	Leu	Tyr	Lys	Thr	Pro	Cys	Thr	Lys	Arg
256		290				295					300					
259	Phe	Glu	Met	Thr	Leu	Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly	Ile	Gly
260	305					310					315					320
263	Asn	Tyr	Gln	Gln	Cys	His	Gln	Ser	Ile	Leu	Glu	Leu	Phe	Asn	Thr	Ser
264				325						330					335	
267	Tyr	Cys	Pro	Tyr	Ser	Gln	Cys	Ala	Phe	Asn	Gly	Ile	Phe	Leu	Pro	Pro
268				340					345					350		
271	Leu	Gln	Gly	Asp	Phe	Gly	Ala	Phe	Ser	Ala	Phe	Tyr	Phe	Val	Met	Lys
272			355					360					365			
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276		370				375					380					
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280	385					390					395					400
283	Tyr	Ala	Gly	Val	Lys	Glu	Lys	Tyr	Leu	Ser	Glu	Tyr	Cys	Phe	Ser	Gly
284				405					410					415		
287	Thr	Tyr	Ile	Leu	Ser	Leu	Leu	Leu	Gln	Gly	Tyr	His	Phe	Thr	Ala	Asp
288				420					425					430		
291	Ser	Trp	Glu	His	Ile	His	Phe	Ile	Gly	Lys	Ile	Gln	Gly	Ser	Asp	Ala
292			435					440					445			
295	Gly	Trp	Thr	Leu	Gly	Tyr	Met	Leu	Asn	Leu	Thr	Asn	Met	Ile	Pro	Ala
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303 Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile Gly Leu
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312 <211> LENGTH: 476
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316 <220> FEATURE:
317 <223> OTHER INFORMATION: Fusion construct of human CD39
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329 Ile Phe Leu Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
330 35 40 45
333 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
334 50 55 60
337 Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
338 65 70 75 80
341 Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
342 85 90 95
345 Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
346 100 105 110
349 Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
350 115 120 125
353 Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
354 130 135 140
357 Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
358 145 150 155 160
361 Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
362 165 170 175
365 Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
366 180 185 190
369 Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
370 195 200 205
373 Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
374 210 215 220
377 Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
378 225 230 235 240
381 Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
382 245 250 255
385 Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
386 260 265 270
389 Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
390 275 280 285
393 Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
394 290 295 300

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/835,147A

DATE: 01/29/2003
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Input Set : A:\2879-US RevsdSeqListing 010303.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; Xaa Pos. 39